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LOGINID:ssspta1652dmr

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2


* * * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1          Web Page for STN Seminar Schedule - N. America
 NEWS  2  NOV 21  CAS patent coverage to include exemplified prophetic
                  substances identified in English-, French-, German-,
                  and Japanese-language basic patents from 2004-present
 NEWS  3  NOV 26  MARPAT enhanced with FSORT command
 NEWS  4  NOV 26  CHEMSAFE now available on STN Easy
 NEWS  5  NOV 26  Two new SET commands increase convenience of STN
                  searching
 NEWS  6  DEC 01  ChemPort single article sales feature unavailable
 NEWS  7  DEC 12  GBFULL now offers single source for full-text
                  coverage of complete UK patent families
 NEWS  8  DEC 17  Fifty-one pharmaceutical ingredients added to PS
 NEWS  9  JAN 06  The retention policy for unread STNmail messages
                  will change in 2009 for STN-Columbus and STN-Tokyo
 NEWS 10  JAN 07  WPIDS, WPINDEX, and WPIX enhanced Japanese Patent
                  Classification Data

 NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
              AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS LOGIN    Welcome Banner and News Items
 NEWS IPC8     For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that
specific topic.

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* * * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 00:49:28 ON 01 FEB 2009

=> index bioscience medicine
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.22       0.22

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
       AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
       CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
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      DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 00:50:04 ON 01 FEB 2009

71 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s (restric?(3a)endonucleas?) or (restric?(3a)enzym?) or
(restric?(3a)modif?(5a)(enzym? or endonucleas? or system?))
         21   FILE ADISCTI
          3   FILE ADISINSIGHT
          7   FILE ADISNEWS
       3845   FILE AGRICOLA
        104   FILE ANABSTR
         42   FILE ANTE
         40   FILE AQUALINE
       1189   FILE AQUASCI
       3479   FILE BIOENG
  9 FILES SEARCHED...
      31117   FILE BIOSIS
      10212   FILE BIOTECHABS
      10212   FILE BIOTECHDS
      17093   FILE BIOTECHNO
 13 FILES SEARCHED...
      10248   FILE CABA
      40802   FILE CAPLUS
        731   FILE CEABA-VTB
         77   FILE CIN
        338   FILE CONFSCI
          3   FILE CROPB
        124   FILE CROPU
         19   FILE DDFB
        133   FILE DDFU
      43989   FILE DGENE
 23 FILES SEARCHED...
       2088   FILE DISSABS
         19   FILE DRUGB
        425   FILE DRUGU
         88   FILE EMBAL
      21832   FILE EMBASE
       9157   FILE ESBIOBASE
 30 FILES SEARCHED...
        363   FILE FROSTI
       1154   FILE FSTA
    2282317   FILE GENBANK
         53   FILE HEALSAFE
       7069   FILE IFIPAT
         11   FILE IMSDRUGNEWS
 39 FILES SEARCHED...
          9   FILE IMSRESEARCH
         20   FILE KOSMET
      17321   FILE LIFESCI
      40206   FILE MEDLINE
        199   FILE NTIS
        348   FILE OCEAN
      11890   FILE PASCAL
 47 FILES SEARCHED...
        164   FILE PCTGEN
          1   FILE PHAR
          1   FILE PHARMAML
         66   FILE PHIN
        640   FILE PROMT
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         1   FILE PROUSDDR
         3   FILE RDISCLOSURE
     20911   FILE SCISEARCH
     10529   FILE TOXCENTER
  58 FILES SEARCHED...
     14486   FILE USGENE
     72194   FILE USPATFULL
        29   FILE USPATOLD
     11872   FILE USPAT2
         1   FILE VETB
  63 FILES SEARCHED...
       144   FILE VETU
        62   FILE WATER
      9109   FILE WPIDS
        62   FILE WPIFV
      9109   FILE WPINDEX
        37   FILE IPA
         4   FILE NAPRALERT
       488   FILE NLDB

  64 FILES HAVE ONE OR MORE ANSWERS,   71 FILES SEARCHED IN STNINDEX

L1   QUE (RESTRIC?(3A) ENDONUCLEAS?) OR (RESTRIC?(3A) ENZYM?) OR (RESTRIC?(3A)
        MODIF?(5A)(ENZYM? OR ENDONUCLEAS? OR SYSTEM?))

=> d rank
F1     2282317   GENBANK
F2       72194   USPATFULL
F3       43989   DGENE
F4       40802   CAPLUS
F5       40206   MEDLINE
F6       31117   BIOSIS
F7       21832   EMBASE
F8       20911   SCISEARCH
F9       17321   LIFESCI
F10      17093   BIOTECHNO
F11      14486   USGENE
F12      11890   PASCAL
F13      11872   USPAT2
F14      10529   TOXCENTER
F15      10248   CABA
F16      10212   BIOTECHABS
F17      10212   BIOTECHDS
F18       9157   ESBIOBASE
F19       9109   WPIDS
F20       9109   WPINDEX
F21       7069   IFIPAT
F22       3845   AGRICOLA
F23       3479   BIOENG
F24       2088   DISSABS
F25       1189   AQUASCI
F26       1154   FSTA
F27        731   CEABA-VTB
F28        640   PROMT
F29        488   NLDB
F30        425   DRUGU
F31        363   FROSTI
F32        348   OCEAN
F33        338   CONFSCI
F34        199   NTIS
F35        164   PCTGEN
F36        144   VETU
```

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F37         133   DDFU
F38         124   CROPU
F39         104   ANABSTR
F40          88   EMBAL
F41          77   CIN
F42          66   PHIN
F43          62   WATER
F44          62   WPIFV
F45          53   HEALSAFE
F46          42   ANTE
F47          40   AQUALINE
F48          37   IPA
F49          29   USPATOLD
F50          21   ADISCTI
F51          20   KOSMET
F52          19   DDFB
F53          19   DRUGB
F54          11   IMSDRUGNEWS
F55           9   IMSRESEARCH
F56           7   ADISNEWS
F57           4   NAPRALERT
F58           3   ADISINSIGHT
F59           3   CROPB
F60           3   RDISCLOSURE
F61           1   PHAR
F62           1   PHARMAML
F63           1   PROUSDDR
F64           1   VETB


=> file f2, f4-f17
COST IN U.S. DOLLARS                          SINCE FILE      TOTAL
                                                   ENTRY    SESSION
FULL ESTIMATED COST                                12.24      12.46

FILE 'USPATFULL' ENTERED AT 01:00:54 ON 01 FEB 2009
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FILE 'USGENE' ENTERED AT 01:00:54 ON 01 FEB 2009
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FILE 'CABA' ENTERED AT 01:00:54 ON 01 FEB 2009
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FILE 'BIOTECHABS' ACCESS NOT AUTHORIZED

FILE 'BIOTECHDS' ENTERED AT 01:00:54 ON 01 FEB 2009
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=> s (restric?(3a)endonucleas?) or (restric?(3a)enzym?) or
(restric?(3a)modif?(5a)(enzym? or endonucleas? or system?))
   7 FILES SEARCHED...
  10 FILES SEARCHED...
L2      330713 (RESTRIC?(3A) ENDONUCLEAS?) OR (RESTRIC?(3A) ENZYM?) OR (RESTRIC
               ?(3A) MODIF?(5A)(ENZYM? OR ENDONUCLEAS? OR SYSTEM?))

=> s l2(s)(specifi? or recog?)(s)(sequenc? or dna?)
   5 FILES SEARCHED...
   9 FILES SEARCHED...
L3       79162 L2(S)(SPECIFI? OR RECOG?)(S)(SEQUENC? OR DNA?)

=> s l3 and (hybrid? or recombinat? or truncat? or transpos?)
L4       49041 L3 AND (HYBRID? OR RECOMBINAT? OR TRUNCAT? OR TRANSPOS?)

=> s l3(s)((two(3a)recognit?(3a)site?) or hsds?)
L5         990 L3(S)((TWO(3A) RECOGNIT?(3A) SITE?) OR HSDS?)

=>
=> s l5 (s)(hybrid? or recombin? or trunca? or or exchang? or transpos? or alter?)
MISSING TERM 'OR OR'
The search profile that was entered contains a logical
operator followed immediately by another operator.

=> s l5 (s)(hybrid? or recombin? or trunca? or exchang? or transpos? or alter?)
   5 FILES SEARCHED...
  11 FILES SEARCHED...
L6         344 L5 (S)(HYBRID? OR RECOMBIN? OR TRUNCA? OR EXCHANG? OR TRANSPOS?
               OR ALTER?)

=> dup rem l6
DUPLICATE IS NOT AVAILABLE IN 'USGENE'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L6
L7          280 DUP REM L6 (64 DUPLICATES REMOVED)

=> s l7(s)half?
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L82(S)HALF?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
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FIELD CODE - 'AND' OPERATOR ASSUMED 'L86(S)HALF?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L88(S)HALF?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L100(S)HALF?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L102(S)HALF?'
L8          14 L7(S) HALF?

=> d ti l8 1-14

L8   ANSWER 1 OF 14  USPATFULL on STN
TI     Small interfering RNA libraries and methods of synthesis and use

L8   ANSWER 2 OF 14  USPATFULL on STN
TI     Nucleic acid and amino acid sequences relating to Enterobacter cloacae
       for diagnostics and therapeutics

L8   ANSWER 3 OF 14  USPATFULL on STN
TI     Differential enzymatic fragmentation by whole genome amplification

L8   ANSWER 4 OF 14  USPATFULL on STN
TI     Differential enzymatic fragmentation

L8   ANSWER 5 OF 14  USPATFULL on STN
TI     Methods for quantitative determination of methylation density in a DNA
       locus

L8   ANSWER 6 OF 14  USPATFULL on STN
TI     Compositions and methods for the therapy and diagnosis of colon cancer

L8   ANSWER 7 OF 14  USPATFULL on STN
TI     Compositions and methods for the therapy and diagnosis of pancreatic
       cancer

L8   ANSWER 8 OF 14  USPATFULL on STN
TI     Nuclease

L8   ANSWER 9 OF 14  USPATFULL on STN
TI     Compositions and methods for the therapy and diagnosis of colon cancer

L8   ANSWER 10 OF 14  USPATFULL on STN
TI     Compositions and methods for the therapy and diagnosis of ovarian cancer

L8   ANSWER 11 OF 14  USPATFULL on STN
TI     Compositions and methods for the therapy and diagnosis of colon cancer

L8   ANSWER 12 OF 14  LIFESCI    COPYRIGHT 2009 CSA on STN
TI   DNA Cleavage by Type III Restriction-modification Enzyme  Eco P15I is
     Independent of Spacer Distance between Two Head to Head Oriented
     Recognition Sites

L8   ANSWER 13 OF 14  LIFESCI    COPYRIGHT 2009 CSA on STN
TI   Generation of new DNA binding specificity by truncation of the type IC
     EcoDXXI hsdS gene

L8    ANSWER 14 OF 14  BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI    Dendrimer based multifunctional composition for treating cancer and
      cardiovascular disease, comprises a dendrimer complex having dendrimers
      comprising different agents e.g. therapeutic and biological monitoring
      agents;
         useful for inflammatory disease and pathogen disease gene therapy,
```

diagnosis and drug target screening

=> d l8 ibib abs 8 12 13

L8 ANSWER 8 OF 14 USPATFULL on STN
ACCESSION NUMBER: 2003:58047 USPATFULL
TITLE: Nuclease
INVENTOR(S): Janulaitis, Arvydas, Vilnius, LITHUANIA
Rimseliene, Renata, Vilnius, LITHUANIA
Lubys, Arvydas, Vilnius, LITHUANIA
PATENT ASSIGNEE(S): Fermentas AB (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 20030040614	A1	20030227
	US 6893854	B2	20050517
APPLICATION INFO.:	US 2001-906768	A1	20010718 (9)

	NUMBER	DATE
PRIORITY INFORMATION:	GB 2000-19744	20000810

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: PILLSBURY WINTHROP, LLP, P.O. BOX 10500, MCLEAN, VA, 22102
NUMBER OF CLAIMS: 17
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 6 Drawing Page(s)
LINE COUNT: 1029
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A process for producing a polynucleotide encoding a restriction endonuclease with an altered specificity, which process comprises:

(a) mutagenising a polynucleotide encoding a restriction endonuclease with specificity for a recognition sequence so as to produce one or more mutated polynucleotides; and

(b) isolating therefrom a polynucleotide encoding a mutated restriction endonuclease with specificity for an altered recognition sequence by selecting a polynucleotide which expresses a restriction endonuclease with methylase specificity for the altered recognition sequence.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L8 ANSWER 12 OF 14 LIFESCI COPYRIGHT 2009 CSA on STN
ACCESSION NUMBER: 2001:107290 LIFESCI
TITLE: DNA Cleavage by Type III Restriction-modification Enzyme Eco P15I is Independent of Spacer Distance between Two Head to Head Oriented Recognition Sites
AUTHOR: Muecke, M.; Reich, S.; Moencke-Buchner, E.; Reuter, M.; Krueger, D.H.*
CORPORATE SOURCE: Institut fuer Virologie, Medizinische Fakultaet (Charite), der Humboldt-Universitaet zu Berlin, D-10098, Berlin, Germany
SOURCE: Journal of Molecular Biology [J. Mol. Biol.], (20010928) vol. 312, no. 4, pp. 687-698.
ISSN: 0022-2836.
DOCUMENT TYPE: Journal
FILE SEGMENT: N; J
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The type III restriction-modification enzyme EcoP15I requires the interaction of two unmethylated, inversely oriented recognition sites 5'-CAGCAG in head to head configuration to allow an efficient DNA cleavage. It has been hypothesized that two convergent DNA-translocating enzyme-substrate complexes interact to form the active cleavage complex and that translocation is driven by ATP hydrolysis. Using a half -automated, fluorescence-based detection method, we investigated how the distance between two inversely oriented recognition sites affects DNA cleavage efficiency. We determined that EcoP15I cleaves DNA efficiently even for two adjacent head to head or tail to tail oriented target sites. Hence, DNA translocation appears not to be required for initiating DNA cleavage in these cases. Furthermore, we report here that EcoP15I is able to cleave single-site substrates. When we analyzed the interaction of EcoP15I with DNA substrates containing adjacent target sites in the presence of non-hydrolyzable ATP analogues, we found that cleavage depended on the hydrolysis of ATP. Moreover, we show that cleavage occurs at only one of the two possible cleavage positions of an interacting pair of target sequences. When EcoP15I bound to a DNA substrate containing one recognition site in the absence of ATP, we observed a 36 nucleotide DNaseI-footprint that is asymmetric on both strands. All of our footprinting experiments showed that the enzyme did not cover the region around the cleavage site. Analyzing a DNA fragment with two head to head oriented recognition sites, EcoP15I protected 27-33 nucleotides around the recognition sequence, including an additional region of 26 bp between both cleavage sites. For all DNA substrates examined, the presence of ATP caused altered footprinting patterns. We assume that the altered patterns are most likely due to a conformational change of the enzyme. Overall, our data further refine the tracking-collision model for type III restriction enzymes. Copyright 2001 Academic Press

L8 ANSWER 13 OF 14 LIFESCI COPYRIGHT 2009 CSA on STN
ACCESSION NUMBER: 97:330 LIFESCI
TITLE: Generation of new DNA binding specificity by truncation of the type IC EcoDXXI hsdS gene
AUTHOR: MacWilliams, M.P.; Bickle, T.A.*
CORPORATE SOURCE: Dep. Microbiol., Biozentrum, Basel Univ., Klingelbergstrasse 70, CH-4056 Basel, Switzerland
SOURCE: EMBO J., (1996) vol. 15, no. 17, pp. 4775-4783. ISSN: 0261-4189.
DOCUMENT TYPE: Journal
FILE SEGMENT: G; J
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The hsdS subunit of a type IC restriction-modification enzyme is responsible for the enzyme's DNA binding specificity. Type I recognition sites are characterized by two defined half -sites separated by a non-specific spacer of defined length. The hsdS subunit contains two independent DNA binding domains, each targeted towards one DNA half-site. We have shown previously that the 5' half of hsdS can code for a functional substitute of the full-length hsdS. Here we demonstrate that the 3' half of the gene, when fused to the appropriate transcriptional and translational start signals, also codes for a peptide which imparts DNA binding specificity to the enzyme. About half the natural hsdS size, the mutant peptide contains a single DNA recognition domain flanked by one copy of each internal repeat found in the

full-length hsdS. Deletion of either repeat sequence
results in loss of activity. Like the 5' hsdS mutant, the 3'
mutant recognizes an interrupted palindrome, GAAYN sub(5)RTTC,
suggesting that two truncated subunits participate in
DNA recognition. Coexpression of the 5' hsdS
mutant and the 3' hsdS mutant along with hsdM regenerates the
wild-type methylation specificity. Thus, there is a free
assortment of subunits in the cell.

```
=> s l2(s)((two(3a)recog?(3a)site?) or hsds? or (half?(3a)site?))
L9        1657 L2(S)((TWO(3A) RECOG?(3A) SITE?) OR HSDS? OR (HALF?(3A) SITE?))


=> s l9(s)(hybrid? or recomb? or trunc? or exch? or transpo? or alter?)
  10 FILES SEARCHED...
L10        500 L9(S)(HYBRID? OR RECOMB? OR TRUNC? OR EXCH? OR TRANSPO? OR
               ALTER?)

=> s l10 and ((modif? or alter? or hybrid?)(3a)(dna? or sequen? or specific? or
(recogn?(3a)site?)))
   1 FILES SEARCHED...
   2 FILES SEARCHED...
   8 FILES SEARCHED...
   9 FILES SEARCHED...
  10 FILES SEARCHED...
  11 FILES SEARCHED...
L11        359 L10 AND ((MODIF? OR ALTER? OR HYBRID?)(3A)(DNA? OR SEQUEN? OR
               SPECIFIC? OR (RECOGN?(3A) SITE?)))

=> dup rem l11
DUPLICATE IS NOT AVAILABLE IN 'USGENE'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L11
L12         314 DUP REM L11 (45 DUPLICATES REMOVED)

=> d ti l12 1-314

L12  ANSWER 1 OF 314  USPATFULL on STN
TI     HOMOLOGOUS RECOMBINATION IN PLANTS

L12  ANSWER 2 OF 314  USPATFULL on STN
TI     Methods and Compositions Involving Polymeric Immunoglobulin Fusion
       Proteins

L12  ANSWER 3 OF 314  USPATFULL on STN
TI     Rabies Virus Vector Systems and Compositions and Methods Thereof

L12  ANSWER 4 OF 314  USPATFULL on STN
TI     Polypeptides from Non-Typeable Haemophilus Influenzae

L12  ANSWER 5 OF 314  USPATFULL on STN
TI     Analysis of methylation using selective adaptor ligation

L12  ANSWER 6 OF 314  USPATFULL on STN
TI     Methods for Identification of Merle Gene

L12  ANSWER 7 OF 314  USPATFULL on STN
TI     Compositions and Methods for Genetic Manipulation and Monitoring of Cell
       Lines

L12  ANSWER 8 OF 314  USPATFULL on STN
```

TI Selection and Enrichment of Proteins Using in vitro Compartmentalization

L12 ANSWER 9 OF 314 USPATFULL on STN
TI OLIGONUCLEOTIDE LINKERS COMPRISING A VARIABLE COHESIVE PORTION AND METHOD FOR THE PREPARATION OF POLYNUCLEOTIDE LIBRARIES BY USING SAID LINKERS

L12 ANSWER 10 OF 314 USPATFULL on STN
TI Attenuated parainfluenza virus (PIV) vaccines

L12 ANSWER 11 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI Expressing a sequence of interest in a plant cell, including a plant, plant part, or plant cell culture comprises providing a cell with a DNA sequence and causing expression of the sequence of interest; recombinant protein produced by vector mediated gene expression in host cell, useful in construction of transgenic plant

L12 ANSWER 12 OF 314 USPATFULL on STN DUPLICATE 1
TI METHODS FOR IDENTIFICATION OF ALPORT SYNDROME

L12 ANSWER 13 OF 314 USPATFULL on STN DUPLICATE 2
TI Nucleic acid and amino acid sequences relating to streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 14 OF 314 USPATFULL on STN DUPLICATE 3
TI Nucleic acid and amino acid sequences relating to Streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 15 OF 314 USPATFULL on STN DUPLICATE 4
TI Nucleic acid and amino acid sequences relating to Streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 16 OF 314 USPATFULL on STN
TI NON-REDUCING SACCHARIDE-FORMING ENZYME, TREHALOSE-RELEASING ENZYME, AND PROCESS FOR PRODUCING SACCHARIDES USING THE ENZYMES

L12 ANSWER 17 OF 314 USPATFULL on STN
TI Group b streptococcus antigens

L12 ANSWER 18 OF 314 USPATFULL on STN
TI Artificial plant minichromosomes

L12 ANSWER 19 OF 314 USPATFULL on STN
TI Methods for assembly of high fidelity synthetic polynucleotides

L12 ANSWER 20 OF 314 USPATFULL on STN
TI Methods and Means for Regulating Gene Expression

L12 ANSWER 21 OF 314 USPATFULL on STN
TI Directed enrichment of genomic DNA for high-throughput sequencing

L12 ANSWER 22 OF 314 USPATFULL on STN
TI NON-REDUCING SACCHARIDE-FORMING ENZYME, TREHALOSE-RELEASING ENZYME, AND PROCESS FOR PRODUCING SACCHARIDES USING THE ENZYMES

L12 ANSWER 23 OF 314 USPATFULL on STN
TI Small interfering RNA libraries and methods of synthesis and use

L12 ANSWER 24 OF 314 USPATFULL on STN
TI Novel modular type II restriction endonuclease, cspci, and the use of modular endonucleases for generating endonucleases with new

specificities

L12 ANSWER 25 OF 314 USPATFULL on STN
TI Targeted integration and expression of exogenous nucleic acid sequences

L12 ANSWER 26 OF 314 USPATFULL on STN
TI Attenuated human-bovine chimeric parainfluenza virus (PIV) vaccines

L12 ANSWER 27 OF 314 USPATFULL on STN
TI Methods for assembly of high fidelity synthetic polynucleotides

L12 ANSWER 28 OF 314 USPATFULL on STN
TI BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VACCINIA REGULATORY GENES AND USES THEREOF

L12 ANSWER 29 OF 314 USPATFULL on STN
TI Process for chromosomal expression of foreign genes in the hsdM region of a methylotrophic microbial host cell

L12 ANSWER 30 OF 314 USPATFULL on STN
TI Methods for genotyping

L12 ANSWER 31 OF 314 USPATFULL on STN
TI Nucleic acid and amino acid sequences relating to Streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 32 OF 314 USPATFULL on STN
TI Nucleic acid and amino acid sequences relating to Streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 33 OF 314 USPATFULL on STN
TI Cell line and methods for determining viral titer

L12 ANSWER 34 OF 314 USPATFULL on STN
TI Insertion sequence-free bacteria

L12 ANSWER 35 OF 314 USPATFULL on STN
TI Bacteria with reduced genome

L12 ANSWER 36 OF 314 USPATFULL on STN
TI Nucleic acid and amino acid sequences relating to Streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 37 OF 314 USPATFULL on STN
TI Evolution of whole cells and organisms by recursive sequence recombination

L12 ANSWER 38 OF 314 USPATFULL on STN
TI Methods for producing polypeptide-tagged collections and capture systems containing the tagged polypeptides

L12 ANSWER 39 OF 314 USPATFULL on STN
TI Isoprenoid biosynthesis

L12 ANSWER 40 OF 314 USPATFULL on STN
TI Methods for monitoring multiple gene expression

L12 ANSWER 41 OF 314 USPATFULL on STN
TI Nucleic acid and amino acid sequences relating to streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 42 OF 314 USPATFULL on STN

TI Nucleic acid and amino acid sequences relating to streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 43 OF 314 USPATFULL on STN
TI Nucleic acid and amino acid sequences relating to Streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 44 OF 314 USPATFULL on STN
TI Plasmids and methods for construction of non-redundant, indexed, saturation, gene-disruption plant and animal libraries

L12 ANSWER 45 OF 314 USPATFULL on STN
TI Attenuated human-bovine chimeric parainfluenza virus(PIV) vaccines

L12 ANSWER 46 OF 314 USPATFULL on STN
TI Non-reducing saccharide-forming enzyme, trehalose-releasing enzyme, and process for producing saccharides using the enzymes

L12 ANSWER 47 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI Juxtaposing sequence tags comprises digesting a DNA adaptor to cleave the target DNA insert to create two sequence tags comprising terminal sequences of the target DNA insert that are attached to the plasmid vector;
juxtaposing sequence tag via DNA adaptor digestion for disease diagnosis and genomics

L12 ANSWER 48 OF 314 USPATFULL on STN DUPLICATE 5
TI Anthranilate synthase gene and method for increasing tryptophan production

L12 ANSWER 49 OF 314 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 6
TI Polypeptide mutagenesis method using transposons containing restriction enzyme recognition sites toward each termini of the encoding DNA target

L12 ANSWER 50 OF 314 USPATFULL on STN
TI Analysis of methylation using nucleic acid arrays

L12 ANSWER 51 OF 314 USPATFULL on STN
TI Accessible polynucleotide libraries and methods of use thereof

L12 ANSWER 52 OF 314 USPATFULL on STN
TI Gram positive bacterial mutants and methods of generating and using such mutants

L12 ANSWER 53 OF 314 USPATFULL on STN
TI Bacteria with reduced genome

L12 ANSWER 54 OF 314 USPATFULL on STN
TI NOVEL POLYNUCLEOTIDES ENCODING USEFUL POLYPEPTIDES IN CORYNEBACTERIUM GLUTAMICUM SSP. LACTOFERMENTUM

L12 ANSWER 55 OF 314 USPATFULL on STN
TI NOVEL POLYNUCLEOTIDES ENCODING USEFUL POLYPEPTIDES IN CORYNEBACTERIUM GLUTAMICUM SSP. LACTOFERMENTUM

L12 ANSWER 56 OF 314 USPATFULL on STN
TI Strain belonging to the genus streptomyces and being capable of producing nemadictin and process for producing nemadictin using the strain

L12 ANSWER 57 OF 314 USPATFULL on STN
TI Methods and compounds for raising antibodies and for screening antibody

repertoires

L12 ANSWER 58 OF 314 USPATFULL on STN
TI Insertion Sequence-Free Bacteria

L12 ANSWER 59 OF 314 USPATFULL on STN
TI Methods for assembly of high fidelity synthetic polynucleotides

L12 ANSWER 60 OF 314 USPATFULL on STN
TI Method for the manufacture of nucleic acid molecules

L12 ANSWER 61 OF 314 USPATFULL on STN
TI Polypeptides and polynucleotides from coagulase-negative staphylococci

L12 ANSWER 62 OF 314 USPATFULL on STN
TI Protein having PDZ domain sequence

L12 ANSWER 63 OF 314 USPATFULL on STN
TI Methods and compositions for elucidating protein expression profiles in cells

L12 ANSWER 64 OF 314 USPATFULL on STN
TI Attenuated human-bovine chimeric parainfluenza virus (PIV) vaccines

L12 ANSWER 65 OF 314 USPATFULL on STN
TI Hybrid and single chain meganucleases and use thereof

L12 ANSWER 66 OF 314 USPATFULL on STN
TI Methods and systems for in silico experimental design and for providing a biotechnology product to a customer

L12 ANSWER 67 OF 314 USPATFULL on STN
TI Effect of treatment with 4,5-dihydroxy-2-cyclopenten-1-one (dhcp) on gene expression and quorum-sensing in bacteria

L12 ANSWER 68 OF 314 USPATFULL on STN
TI Peptides for metal ion affinity chromatography

L12 ANSWER 69 OF 314 USPATFULL on STN
TI Analysis of mixtures of nucleic acid fragments

L12 ANSWER 70 OF 314 USPATFULL on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof

L12 ANSWER 71 OF 314 USPATFULL on STN
TI Methods of producing mutant polynucleotides

L12 ANSWER 72 OF 314 USPATFULL on STN
TI Sequence specific recombinase-based methods for producing intron containing vectors and compositions for use in practicing the same

L12 ANSWER 73 OF 314 USPATFULL on STN
TI Isoprenoid biosynthesis

L12 ANSWER 74 OF 314 USPATFULL on STN
TI Nucleic acid and amino acid sequences relating to Enterobacter cloacae for diagnostics and therapeutics

L12 ANSWER 75 OF 314 USPATFULL on STN
TI Protein having PDZ domain sequence

L12 ANSWER 76 OF 314 USPATFULL on STN
TI Cystic fibrosis gene

L12 ANSWER 77 OF 314 USPAT2 on STN
TI Nucleic acid and amino acid sequences relating to Streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 78 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI New isolated nucleotide sequence of pgm gene of a Brucella bacterium modified by a partial deletion of the sequence coding for phosphoglucomutase, useful for producing vaccines for treating brucellosis;
recombinant vaccine preparation via attenuated bacterium strain for use in disease therapy

L12 ANSWER 79 OF 314 LIFESCI COPYRIGHT 2009 CSA on STN
TI Site-specific labeling of supercoiled DNA

L12 ANSWER 80 OF 314 USPATFULL on STN DUPLICATE 7
TI Differential enzymatic fragmentation by whole genome amplification

L12 ANSWER 81 OF 314 USPATFULL on STN
TI 2', 5'-oligoadenylate phosphodiesterase

L12 ANSWER 82 OF 314 USPATFULL on STN
TI Novel oligonucleotide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids

L12 ANSWER 83 OF 314 USPATFULL on STN
TI Transposon

L12 ANSWER 84 OF 314 USPATFULL on STN
TI Generation and application of standardized universal libraries

L12 ANSWER 85 OF 314 USPATFULL on STN
TI Nucleic acid molecules containing recombination sites and methods of using the same

L12 ANSWER 86 OF 314 USPATFULL on STN
TI Targeted chromosomal mutagenasis using zinc finger nucleases

L12 ANSWER 87 OF 314 USPATFULL on STN
TI Analysis of methylation status using nucleic acid arrays

L12 ANSWER 88 OF 314 USPATFULL on STN
TI Differential enzymatic fragmentation

L12 ANSWER 89 OF 314 USPATFULL on STN
TI Analysis of methylation status using oligonucleotide arrays

L12 ANSWER 90 OF 314 USPATFULL on STN
TI Methods for quantitative determination of methylation density in a DNA locus

L12 ANSWER 91 OF 314 USPATFULL on STN
TI Method for comprehensive identification of cell lineage specific genes

L12 ANSWER 92 OF 314 USPATFULL on STN
TI Tryparedoxin, expression plasmid, process of preparation, method of use, test kit and pharmaceutical composition

L12 ANSWER 93 OF 314 USPATFULL on STN

TI Nucleic acid and amino acid sequences relating to streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 94 OF 314 USPATFULL on STN
TI Nucleotide sequence of the haemophilus influenzae Rd genome, fragments thereof, and uses thereof

L12 ANSWER 95 OF 314 USPATFULL on STN
TI Methods and compositions for detecting promoter activity and expressing fusion proteins

L12 ANSWER 96 OF 314 USPATFULL on STN
TI Cloning vectors and method for molecular cloning

L12 ANSWER 97 OF 314 USPATFULL on STN
TI Methods for insertion of nucleic acids into circular vectors

L12 ANSWER 98 OF 314 USPATFULL on STN
TI Systems for capture and analysis of biological particles and methods using the systems

L12 ANSWER 99 OF 314 USPATFULL on STN
TI Mapping genomic rearrangements

L12 ANSWER 100 OF 314 USPATFULL on STN
TI Concurrent enzymatic polynucleotide synthesis and detectable signal generation

L12 ANSWER 101 OF 314 USPATFULL on STN
TI Methods of diagnosing and treating hepatic cell proliferative disorders

L12 ANSWER 102 OF 314 USPATFULL on STN
TI Analysis of methylation status using oligonucleotide arrays

L12 ANSWER 103 OF 314 USPATFULL on STN
TI Plant promoter and method for gene expression using said promoter

L12 ANSWER 104 OF 314 USPATFULL on STN
TI Cystic fibrosis gene

L12 ANSWER 105 OF 314 USPAT2 on STN
TI Nucleic acid amplification method

L12 ANSWER 106 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI New pure Type IIG restriction endonuclease obtainable from Citrobacter species or from Escherichia coli, useful for generating restriction endonucleases with new specificities;
for use in genetic engineering

L12 ANSWER 107 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI Identifying a conditional essential gene of an organism, useful for manufacturing a medicament for vaccinating a human or animal, comprises providing a library of transposon mutants of the organism;
involving vector-mediated gene transfer and expression in host cell
for use in therapy and recombinant vaccine preparation

L12 ANSWER 108 OF 314 USPATFULL on STN DUPLICATE 8
TI Group b streptococcus antigens and corresponding dna fragments

L12 ANSWER 109 OF 314 USPATFULL on STN DUPLICATE 9
TI Novel polynucleotides encoding useful polypeptides in corynebacterium glutamicum SSP. lactofermentum

L12 ANSWER 110 OF 314 USPATFULL on STN DUPLICATE 10
TI Use of multiple recombination sites with unique specificity in recombinational cloning

L12 ANSWER 111 OF 314 USPATFULL on STN DUPLICATE 11
TI NUCLEOTIDE SEQUENCE OF THE HAEMOPHILUS INFLUENZAE RD GENOME, FRAGMENTS THEREOF, AND USES THEREOF

L12 ANSWER 112 OF 314 USPATFULL on STN DUPLICATE 12
TI Proteins and polypeptides from coagulaslase-negative staphylococci

L12 ANSWER 113 OF 314 USPATFULL on STN DUPLICATE 13
TI Non-mevalonate isoprenoid pathway

L12 ANSWER 114 OF 314 USPATFULL on STN
TI Use of site specific recombination to prepare molecular markers

L12 ANSWER 115 OF 314 USPATFULL on STN
TI Methods and compositions relating to 5'-chimeric ribonucleic acids

L12 ANSWER 116 OF 314 USPATFULL on STN
TI Viral vectors containing recombination sites

L12 ANSWER 117 OF 314 USPATFULL on STN
TI Methods for producing polypeptide-tagged collections and capture systems containing the tagged polypeptides

L12 ANSWER 118 OF 314 USPATFULL on STN
TI Subscription based systems, methods and components for providing genomic and proteomic products and services

L12 ANSWER 119 OF 314 USPATFULL on STN
TI Method for high throughput elucidation of transcriptional profiles and genome annotation

L12 ANSWER 120 OF 314 USPATFULL on STN
TI Antigens of group b streptococcus and corresponding dna fragments

L12 ANSWER 121 OF 314 USPATFULL on STN
TI Oligonucleotide linkers comprising a variable cohesive portion and method for the praparation of polynucleotide libraries by using said linkers

L12 ANSWER 122 OF 314 USPATFULL on STN
TI Methods for treating or preventing infections from coagulase-negative staphylococci

L12 ANSWER 123 OF 314 USPATFULL on STN
TI Nucleotide sequences of moraxella catarrhalis genome

L12 ANSWER 124 OF 314 USPATFULL on STN
TI Human complement C3-binding protein from streptococcus pneumoniae

L12 ANSWER 125 OF 314 USPATFULL on STN
TI Novel recombinant xylanases derived from anaerobic fungi, and the relevant sequences, expression vectors and hosts

L12 ANSWER 126 OF 314 USPATFULL on STN
TI Use of collections of binding sites for sample profiling and other applications

L12 ANSWER 127 OF 314 USPATFULL on STN
TI Antibodies to polypeptides from coagulase-negative staphylococci

L12 ANSWER 128 OF 314 USPATFULL on STN
TI Nucleotide sequence of the haemophilus influenza Rd genome, fragments thereof, and uses thereof

L12 ANSWER 129 OF 314 USPATFULL on STN
TI Modification of plant cell wall component and method of regulating development differentiation

L12 ANSWER 130 OF 314 USPATFULL on STN
TI Method for the identification of essential and conditional essential genes

L12 ANSWER 131 OF 314 USPATFULL on STN
TI Molecular diagnosis of bactermia

L12 ANSWER 132 OF 314 USPATFULL on STN
TI Hybrid and single chain meganucleases and use thereof

L12 ANSWER 133 OF 314 USPATFULL on STN
TI DNA sequences, recombinant DNA molecules and processes for producing human interferon-like polypeptides

L12 ANSWER 134 OF 314 USPATFULL on STN
TI Methods for insertion of nucleic acids into circular vectors

L12 ANSWER 135 OF 314 USPATFULL on STN
TI Nucleic acid and amino acid sequences relating to Streptococcus pneumoniae for diagnostics and therapeutics

L12 ANSWER 136 OF 314 USPATFULL on STN
TI Cystic fibrosis gene

L12 ANSWER 137 OF 314 USPATFULL on STN
TI Methods of diagnosing and treating hepatic cell proliferative disorders

L12 ANSWER 138 OF 314 USPATFULL on STN
TI Human complement C3-degrading protein from Streptococcus pneumoniae

L12 ANSWER 139 OF 314 USPAT2 on STN
TI NCC2705--the genome of a bifidobacterium

L12 ANSWER 140 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI Preparing small interfering RNA library for treating e.g. cancer, by producing random oligoDNAs that can be cloned into vectors containing site-specific recombinase sites for generating inverted repeats of the sequence in host cells;
for use in cancer prevention, gene therapy, RNA interference and functional genomics

L12 ANSWER 141 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI Identifying sequences that express short interfering RNA, useful for knock down of selected genes, by transforming cells with bank of short oligonucleotides and selection for expression of two reporter genes;
short oligonucleotide identification for short interfering RNA expression and specific gene knock down

L12 ANSWER 142 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI Identifying, analyzing and/or cloning nucleic acid isoforms, useful for preparing a probe, diagnosing a disease, or assessing responsiveness of a

patient to a treatment, comprises preparing complementary nucleic acid isoforms;
DNA isoform cloning and DNA probe for use in disease diagnosis

L12 ANSWER 143 OF 314 USPATFULL on STN DUPLICATE 14
TI Binary vectors for the improved transformation of plants systems

L12 ANSWER 144 OF 314 USPATFULL on STN DUPLICATE 15
TI Nucleic acid transfer vector for the introduction of nucleic acid into the DNA of a cell

L12 ANSWER 145 OF 314 USPATFULL on STN DUPLICATE 16
TI Bacteria with reduced genome

L12 ANSWER 146 OF 314 USPATFULL on STN DUPLICATE 17
TI Sequence specific recombinase-based methods for producing intron containing vectors and compositions for use in practicing the same

L12 ANSWER 147 OF 314 USPATFULL on STN DUPLICATE 18
TI Site specific recombinase based method for producing adenoviral vectors

L12 ANSWER 148 OF 314 USPATFULL on STN DUPLICATE 19
TI Nuclease

L12 ANSWER 149 OF 314 USPATFULL on STN DUPLICATE 20
TI Recombinase-based methods for producing expression vectors and compositions for use in practicing the same

L12 ANSWER 150 OF 314 USPATFULL on STN
TI Novel group B streptococcus antigens

L12 ANSWER 151 OF 314 USPATFULL on STN
TI Method for carrying out the parallel sequencing of a nucleic acid mixture on a surface

L12 ANSWER 152 OF 314 USPATFULL on STN
TI 207 human secreted proteins

L12 ANSWER 153 OF 314 USPATFULL on STN
TI Regulators of bacterial virulence factor expression

L12 ANSWER 154 OF 314 USPATFULL on STN
TI Anthranilate synthase gene and method for increasing tryptophan production

L12 ANSWER 155 OF 314 USPATFULL on STN
TI Compositions and methods for the therapy and diagnosis of colon cancer

L12 ANSWER 156 OF 314 USPATFULL on STN
TI Novel oligonucleotide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids

L12 ANSWER 157 OF 314 USPATFULL on STN
TI Evolution of whole cells and organisms by recursive sequence recombination

L12 ANSWER 158 OF 314 USPATFULL on STN
TI Collections of binding proteins and tags and uses thereof for nested sorting and high throughput screening

L12 ANSWER 159 OF 314 USPATFULL on STN
TI High throughput method for identification of sequence tags

L12 ANSWER 160 OF 314 USPATFULL on STN
TI Attenuated human-bovine chimeric parainfluenza virus (PIV) vaccines

L12 ANSWER 161 OF 314 USPATFULL on STN
TI Tryparedoxin, expression plasmid, process of production, method of use, test kit, and pharmaceutical composition

L12 ANSWER 162 OF 314 USPATFULL on STN
TI Compositions and methods for the therapy and diagnosis of pancreatic cancer

L12 ANSWER 163 OF 314 USPATFULL on STN
TI Human genes and gene expression products

L12 ANSWER 164 OF 314 USPATFULL on STN
TI NOVEL GROUP B STREPTOCOCCUS ANTIGENS

L12 ANSWER 165 OF 314 USPATFULL on STN
TI Cell type specific gene transfers using retroviral vectors containing antibody-envelope fusion proteins and wild-type envelope fusion proteins

L12 ANSWER 166 OF 314 USPATFULL on STN
TI Polypeptides and polynucleotides from coagulase-negative staphylococci

L12 ANSWER 167 OF 314 USPATFULL on STN
TI Nucleic acids encoding 3-ketoacyl-ACP reductase from Moraxella catarrahalis

L12 ANSWER 168 OF 314 USPATFULL on STN
TI Method for in vitro amplification of circular DNA

L12 ANSWER 169 OF 314 USPATFULL on STN
TI Assay for detecting apoptotic cells

L12 ANSWER 170 OF 314 USPATFULL on STN
TI Nucleic acid and amino acid sequences relating to Acinetobacter baumannii for diagnostics and therapeutics

L12 ANSWER 171 OF 314 USPATFULL on STN
TI Nucleotide sequence of the mycoplasma genitalium genome, fragments thereof, and uses thereof

L12 ANSWER 172 OF 314 USPATFULL on STN
TI Cell type specific gene transfer using retroviral vectors containing antibody-envelope fusion proteins and wild-type envelope fusion proteins

L12 ANSWER 173 OF 314 USPATFULL on STN
TI Nucleotide sequence of the Haemophilus influenzae Rd genome, fragments thereof, and uses thereof

L12 ANSWER 174 OF 314 USPATFULL on STN
TI Method of mapping restriction sites in polynucleotides

L12 ANSWER 175 OF 314 USPATFULL on STN
TI Nucleotide sequence of the Haemophilus influenzae Rd genome, fragments thereof, and uses thereof

L12 ANSWER 176 OF 314 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
TI Distribution of Helicobacter pylori 51-specific genes on other Korean isolates of Helicobacter pylori.

L12 ANSWER 177 OF 314 USPATFULL on STN DUPLICATE 21
TI Anthranilate synthase gene and method of use thereof for conferring tryptophan overproduction

L12 ANSWER 178 OF 314 USPATFULL on STN DUPLICATE 22
TI Use of multiple recombination sites with unique specificity in recombinational cloning

L12 ANSWER 179 OF 314 USPATFULL on STN DUPLICATE 23
TI Soluble single chain T cell receptors

L12 ANSWER 180 OF 314 USPATFULL on STN
TI Bifunctional fusion proteins formed from hirudin and TAP

L12 ANSWER 181 OF 314 USPATFULL on STN
TI Compositions and methods for the therapy and diagnosis of colon cancer

L12 ANSWER 182 OF 314 USPATFULL on STN
TI Fungal target genes and methods to identify those genes

L12 ANSWER 183 OF 314 USPATFULL on STN
TI Collections of binding proteins and tags and uses thereof for nested sorting and high throughput screening

L12 ANSWER 184 OF 314 USPATFULL on STN
TI Compositions and methods for the therapy and diagnosis of ovarian cancer

L12 ANSWER 185 OF 314 USPATFULL on STN
TI Compositions and methods for the therapy and diagnosis of colon cancer

L12 ANSWER 186 OF 314 USPATFULL on STN
TI Tryparedoxin, expression plasmid, process of production, method of use, test kit, and pharmaceutical composition

L12 ANSWER 187 OF 314 USPATFULL on STN
TI Identification of congenital stationary night blindness in dogs

L12 ANSWER 188 OF 314 USPATFULL on STN
TI Recombinase-based methods for producing expression vectors and compositions for use in practicing the same

L12 ANSWER 189 OF 314 USPATFULL on STN
TI Computer readable genomic sequence of Haemophilus influenzae Rd, fragments thereof, and uses thereof

L12 ANSWER 190 OF 314 USPATFULL on STN
TI cDNAs coding for members of the carcinoembryonic antigen family

L12 ANSWER 191 OF 314 USPAT2 on STN
TI Methods for monitoring multiple gene expression

L12 ANSWER 192 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI New bacteriophage or plasmid cloning vectors, useful for in vitro or in vivo cloning nucleic acid inserts of interest used as tools in molecular genetic research;
vector-mediated reporter gene transfer and expression in host cell for gene analysis

L12 ANSWER 193 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI Determining a fraction of DNA molecules hemi-methylated at specific CpG dinucleotide sequence in a palindromic CpG methylation site, comprises

digesting DNA sample with an excess of methylation-sensitive restriction endonuclease;
DNA primer and polymerase chain reaction for methylation status evaluation

L12 ANSWER 194 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI Novel oligonucleotide linker or population of linkers for preparing polynucleotide libraries, comprises an oligonucleotide fixed portion and an oligonucleotide variable portion;
DNA primer and DNA sequencing for target ssDNA detection

L12 ANSWER 195 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI Novel adaptor sequences for rapid joining with a target nucleic acid sequence, comprise topoisomerase recognition/cleavage sequence and a functional group or encoded functionality;
DNA adaptor for polymerase chain reaction and target genome or DNA detection

L12 ANSWER 196 OF 314 BIOTECHNO COPYRIGHT 2009 Elsevier Science B.V. on STN
TI Identification of the Staphylococcus aureus etd pathogenicity island which encodes a novel exfoliative toxin, ETD, and EDIN-B

L12 ANSWER 197 OF 314 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
TI Type I restriction-modification systems from Lactobacillus delbrueckii subsp. lactis.

L12 ANSWER 198 OF 314 USPATFULL on STN
TI Oligonucleotide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids

L12 ANSWER 199 OF 314 USPATFULL on STN
TI Pullulanase expression constructs containing α-amylase promoter and leader sequences

L12 ANSWER 200 OF 314 USPATFULL on STN
TI Anthranilate synthase gene and method of use thereof for conferring tryptophan overproduction

L12 ANSWER 201 OF 314 USPATFULL on STN
TI Auxiliary genes and proteins of methicillin resistant bacteria and antagonists thereof

L12 ANSWER 202 OF 314 USPATFULL on STN
TI Method for introducing unidirectional nested deletions

L12 ANSWER 203 OF 314 USPATFULL on STN
TI Compositions, methods and kits for identifying naturally occurring RNA sequences having affinity for RNA-binding proteins

L12 ANSWER 204 OF 314 USPATFULL on STN
TI Compositions, methods, kits and apparatus for determining the presence or absence of target molecules

L12 ANSWER 205 OF 314 USPATFULL on STN
TI Identification of congenital stationary night blindness in dogs

L12 ANSWER 206 OF 314 USPATFULL on STN
TI Cystic fibrosis gene

L12 ANSWER 207 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI Identification of a preferred liver transplant donor for donation to

patients with hepatitis C comprises determining the presence or absence of altered activity in a tumor necrosis factor;
DNA primer and polymerase chain reaction for tumor necrosis factor polymorphism detection, genotyping and tranplantation

L12 ANSWER 208 OF 314 BIOTECHNO COPYRIGHT 2009 Elsevier Science B.V. on STN
TI DNA cleavage by type III restriction-modification enzyme EcoP15I is independent of spacer distance between two head to head oriented recognition sites

L12 ANSWER 209 OF 314 USPATFULL on STN
TI Auxiliary genes and proteins of methicillin resistant bacteria and antagonists thereof

L12 ANSWER 210 OF 314 USPATFULL on STN
TI Anthranilate synthase gene and method of use thereof for conferring tryptophan overproduction

L12 ANSWER 211 OF 314 USPATFULL on STN
TI Cleaved amplified modified polymorphic sequence detection methods

L12 ANSWER 212 OF 314 USPATFULL on STN
TI Method of sorting a mixture of nucleic acid strands on a binary array

L12 ANSWER 213 OF 314 USPATFULL on STN
TI Auxiliary genes and proteins of methicillin resistant bacteria and antagonists thereof

L12 ANSWER 214 OF 314 USPATFULL on STN
TI Compositions, methods, kits and apparatus for determining the presence or absence of protein component of telomerase enzyme

L12 ANSWER 215 OF 314 USPATFULL on STN
TI Plant promoter and method for gene expression using said promoter

L12 ANSWER 216 OF 314 USPATFULL on STN
TI cDNAs coding for members of the carcinoembryonic antigen family

L12 ANSWER 217 OF 314 USPATFULL on STN
TI Antibody preparations specifically binding to unique determinants of CEA antigens or fragments thereof and use of the antibody preparations in immunoassays

L12 ANSWER 218 OF 314 USPATFULL on STN
TI Auxiliary genes and proteins of methicillin resistant bacteria and antagonists thereof

L12 ANSWER 219 OF 314 USPATFULL on STN
TI Assay for detecting apoptotic cells

L12 ANSWER 220 OF 314 LIFESCI COPYRIGHT 2009 CSA on STN DUPLICATE 24
TI Broad-Range Bacteriophage Resistance in Streptococcus thermophilus by Insertional Mutagenesis

L12 ANSWER 221 OF 314 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 25
TI Characterization of a Novel Plasmid-Encoded HsdS Subunit, S.LlaW12I, from Lactococcus lactis W12

L12 ANSWER 222 OF 314 USPATFULL on STN
TI Introns and exons of the cystic fibrosis gene and mutations thereof

L12 ANSWER 223 OF 314 USPATFULL on STN
TI Compositions, methods, kits and apparatus for determining the presence or absence of target molecules

L12 ANSWER 224 OF 314 USPATFULL on STN
TI Methods for screening for mutations at various positions in the introns and exons of the cystic fibrosis gene

L12 ANSWER 225 OF 314 USPATFULL on STN
TI Compound microsatellite primers for the detection of genetic polymorphisms

L12 ANSWER 226 OF 314 USPATFULL on STN
TI Fatty acid desaturase genes from plants

L12 ANSWER 227 OF 314 USPATFULL on STN
TI Cell type specific gene transfer using retroviral vectors containing antibody-envelope fusion proteins and wild-type envelope fusion proteins

L12 ANSWER 228 OF 314 USPATFULL on STN
TI Methods and materials for producing gene libraries

L12 ANSWER 229 OF 314 USPATFULL on STN
TI In vitro ligation of foreign DNA into large eukaryotic viruses

L12 ANSWER 230 OF 314 CAPLUS COPYRIGHT 2009 ACS on STN
TI Phage resistance genes hsdR, hsdM and hsdS of lactic acid bacteria and recombinant bacteria producing the restriction endonuclease, methylase and HsdS

L12 ANSWER 231 OF 314 BIOTECHNO COPYRIGHT 2009 Elsevier Science B.V. on STN
TI Regulation of endonuclease activity by proteolysis prevents breakage of unmodified bacterial chromosomes by type I restriction enzymes

L12 ANSWER 232 OF 314 CAPLUS COPYRIGHT 2009 ACS on STN
TI DNA restriction dependent on two recognition sites: activities of the SfiI restriction-modification system in Escherichia coli

L12 ANSWER 233 OF 314 USPATFULL on STN
TI CDNA coding for carcinoembryonic antigen

L12 ANSWER 234 OF 314 USPATFULL on STN
TI Multimeric, recombinant urease vaccine

L12 ANSWER 235 OF 314 USPATFULL on STN
TI Method for producing lipolytic enzymes using transformed Pseudomonas

L12 ANSWER 236 OF 314 USPATFULL on STN
TI Polynucleotide sizing reagent

L12 ANSWER 237 OF 314 USPATFULL on STN
TI Methods of detecting cystic fibrosis gene by nucleic acid hybridization

L12 ANSWER 238 OF 314 USPATFULL on STN
TI Detection of nucleic acids in cells by thermophilic strand displacement amplification

L12 ANSWER 239 OF 314 USPATFULL on STN
TI Strand displacement amplification using thermophilic enzymes

L12 ANSWER 240 OF 314 USPATFULL on STN
TI Detection of nucleic acids in cells by thermophilic strand displacement

amplification

L12 ANSWER 241 OF 314 USPATFULL on STN
TI Isolated protein from Eimeria useful as a cross species vaccine

L12 ANSWER 242 OF 314 USPATFULL on STN
TI Nicking of DNA using boronated nucleotides

L12 ANSWER 243 OF 314 USPATFULL on STN
TI Method of inhibiting cell growth with the P.sub.2U receptor

L12 ANSWER 244 OF 314 USPATFULL on STN
TI Neuroblastoma-associated regulator gene

L12 ANSWER 245 OF 314 USPATFULL on STN
TI Methods and materials for producing gene libraries

L12 ANSWER 246 OF 314 USPATFULL on STN
TI Neuroblastoma-associated regulator gene

L12 ANSWER 247 OF 314 USPATFULL on STN
TI Strand displacement amplification using thermophilic enzymes

L12 ANSWER 248 OF 314 USPATFULL on STN
TI Detection of nucleic acids in cells by thermophilic strand displacement amplification

L12 ANSWER 249 OF 314 USPATFULL on STN
TI Methods of detecting compounds which bind to the P.sub.2U receptor

L12 ANSWER 250 OF 314 USPATFULL on STN
TI DNA Encoding the human P.sub.2U receptor and null cells expressing P.sub.2U receptors

L12 ANSWER 251 OF 314 USPATFULL on STN
TI Efficient directional genetic cloning system

L12 ANSWER 252 OF 314 LIFESCI COPYRIGHT 2009 CSA on STN DUPLICATE 26
TI Selection of non-specific DNA cleavage sites by the type IC restriction endonuclease EcoR124I

L12 ANSWER 253 OF 314 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 27
TI The hsd loci of Mycoplasma pulmonis: organization, rearrangements and expression of genes

L12 ANSWER 254 OF 314 USPATFULL on STN
TI CDNA coding for carcinoembryonic antigen

L12 ANSWER 255 OF 314 USPATFULL on STN
TI Compositions and methods for making lipolytic enzymes

L12 ANSWER 256 OF 314 BIOTECHNO COPYRIGHT 2009 Elsevier Science B.V. on STN
TI The methylation pattern of a cytosine DNA-methyltransferase gene Arabidopsis thaliana plants

L12 ANSWER 257 OF 314 USPATFULL on STN
TI Industrial yeast comprising an integrated glucoamylase gene

L12 ANSWER 258 OF 314 CAPLUS COPYRIGHT 2009 ACS on STN
TI Highly efficient eukaryotic gene expression vectors for peptide secretion

L12 ANSWER 259 OF 314 USPATFULL on STN

TI Expression and purification of recombinant soluble tissue factor

L12 ANSWER 260 OF 314 USPATFULL on STN
TI 25 KD coccidial antigen of eimeria tenella

L12 ANSWER 261 OF 314 USPATFULL on STN
TI Molecular cloning and expression of gene encoding lipolytic enzyme

L12 ANSWER 262 OF 314 USPATFULL on STN
TI cDNA coding for carcinoembryonic antigen (CEA)

L12 ANSWER 263 OF 314 USPATFULL on STN
TI Process and nucleic acid construct for producing reagent complexes useful in determining target nucleotide sequences

L12 ANSWER 264 OF 314 USPATFULL on STN
TI CDNAS coding for members of the carcinoembryonic antigen family

L12 ANSWER 265 OF 314 USPATFULL on STN
TI Recombinant baculovirus

L12 ANSWER 266 OF 314 USPATFULL on STN
TI DNA sequencing vector with reversible insert

L12 ANSWER 267 OF 314 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 28
TI Macroevolution by transposition: Drastic modification of DNA recognition by a type I restriction enzyme following Tn5 transposition

L12 ANSWER 268 OF 314 USPATFULL on STN
TI CDNAS coding for members of the carcinoembryonic antigen family

L12 ANSWER 269 OF 314 CAPLUS COPYRIGHT 2009 ACS on STN
TI Recombination of constant and variable modules alters DNA sequence recognition by type IC restriction - modification enzymes

L12 ANSWER 270 OF 314 USPATFULL on STN
TI Recombinant DNA molecules for producing terminal transferase-like polypeptides

L12 ANSWER 271 OF 314 USPATFULL on STN
TI Modified microorganisms and method of preparing and using same

L12 ANSWER 272 OF 314 USPATFULL on STN
TI Method and vector organism for controlled accumulation of cloned heterologous gene products in Bacillus subtilis

L12 ANSWER 273 OF 314 USPATFULL on STN
TI Yeast promoter and process for preparing heterologous protein

L12 ANSWER 274 OF 314 USPATFULL on STN
TI Hybrid interferons, their use as pharmaceutical compositions and as intermediate products for the preparation of antibodies and the use thereof and processes for preparing them

L12 ANSWER 275 OF 314 USPATFULL on STN
TI Novel expression control sequences

L12 ANSWER 276 OF 314 USPATFULL on STN
TI Method for cloning genes

L12 ANSWER 277 OF 314 USPATFULL on STN
TI Assay, reagent and kit employing nucleic acid strand displacement and restriction endonuclease cleavage

L12 ANSWER 278 OF 314 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 29
TI Evolution of DNA sequence specificity in type I restriction enzymes

L12 ANSWER 279 OF 314 USPATFULL on STN DUPLICATE 30
TI Methods and materials for obtaining microbial expression of polypeptides including bovine prolactin

L12 ANSWER 280 OF 314 USPATFULL on STN
TI Method and vector organism for controlled accumulation of cloned heterologous gene products in Bacillus subtilis

L12 ANSWER 281 OF 314 USPATFULL on STN
TI Recombinant DNA molecules and their use in producing human interferon-like polypeptides

L12 ANSWER 282 OF 314 BIOTECHNO COPYRIGHT 2009 Elsevier Science B.V. on STN
TI EcoA and EcoE: Alternatives to the EcoK family of type I restriction and modification systems of Escherichia coli

L12 ANSWER 283 OF 314 LIFESCI COPYRIGHT 2009 CSA on STN DUPLICATE 31
TI Genetic recombination can generate altered restriction specificity.

L12 ANSWER 284 OF 314 USPATFULL on STN
TI Method for cloning genes

L12 ANSWER 285 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
TI Structural homologies among type I restriction-modification system; an investigation to determine whether the systems are related in Enterobacteriaceae and Escherichia coli K12

L12 ANSWER 286 OF 314 USPATFULL on STN
TI Modified microorganisms and method of preparing and using same

L12 ANSWER 287 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 288 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 289 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 290 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 291 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 292 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 293 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 294 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 295 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 296 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 297 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 298 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 299 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 300 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 301 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 302 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 303 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 304 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 305 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 306 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 307 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 308 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and

methods of use thereof (PublishedApplication)

L12 ANSWER 309 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 310 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 311 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 312 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 313 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

L12 ANSWER 314 OF 314 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Methods for producing a paired tag from a nucleic acid sequence and methods of use thereof (PublishedApplication)

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L12 ANSWER 106 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
ACCESSION NUMBER: 2005-29788 BIOTECHDS
TITLE: New pure Type IIG restriction endonuclease obtainable from Citrobacter species or from Escherichia coli, useful for generating restriction endonucleases with new specificities; for use in genetic engineering
AUTHOR: MORGAN R; WILSON G; LUNNEN K; HEITER D; BENNER J; NKENFOU C N; PICONE S
PATENT ASSIGNEE: NEW ENGLAND BIOLABS INC
PATENT INFO: WO 2005094516 13 Oct 2005
APPLICATION INFO: WO 2005-US9824 23 Mar 2005
PRIORITY INFO: US 2004-555796 24 Mar 2004; US 2004-555796 24 Mar 2004
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2005-714328 [73]
AN 2005-29788 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - A substantially pure Type IIG restriction endonuclease (I) obtainable from Citrobacter sp. 2144 (NEB#1398) (American Type Culture Collection (ATCC) Patent Accession Number PTA-5846) or from Escherichia coli NEB#1554 (ATCC Patent Accession Number PTA-5887), is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) an isolated DNA obtainable from Citrobacter sp. 2144 (NEB (2) 1398) (ATCC Patent Accession Number PTA-5846) or from E.coli NEB (3) 1554 (ATCC Patent Accession Number PTA-5887) and encoding (I), where the DNA comprises a first DNA segment expressing an endonuclease and methyl transferase catalytic function and a second DNA segment encoding a sequence specificity function of the restriction endonuclease, where the first and second DNA segments comprise one or more DNA molecules; (4) a recombinant DNA vector comprising at least one of first DNA segment coding for the restriction and modification domains of CspCI

restriction endonuclease and a second segment coding for the specificity domain of the restriction endonuclease; (5) a host cell (II) transformed with a first DNA segment coding for the restriction and modification domains of CspCI restriction endonuclease and a second segment coding for the specificity domain of the restriction endonuclease, where the first DNA segment and the second DNA segment are contained with one or more DNA vectors; (6) preparing (I); and (7) making (M1) Type II restriction endonuclease having an altered specificity comprising: (a) selecting a restriction endonuclease from a set of enzymes, where each enzyme in the set is characterized by a modular structure having a specificity subunit and a catalytic subunit, the specificity subunit further comprising N-terminal domain for binding one half site of a bipartite recognition sequence and a C-terminal domain for binding a second half site of the bipartite recognition sequence; (b) modifying the specificity subunit; and (c) obtaining the Type II restriction endonuclease with altered specificity.

BIOTECHNOLOGY - Preparation: Preparing (I), involves cultivating a sample of Citrobacter sp. 2144 (NEB#1398) or (II) under conditions favoring the production of the endonuclease, and purifying the endonuclease (claimed). Preferred Endonuclease: (I) Is capable of recognizing at least one sequence chosen (SEQ ID No: 32-35), and cleaving the DNA on both sides of the recognition sequence. Preferred Method: In (M1), modifying the specificity subunit further comprises: (a) substituting the N-terminal domain with a second C-terminal domain or substituting the C-terminal domain with a second N-terminal domain; (b) substituting the N-terminal domain or the C-terminal domain or both N-terminal and C-terminal domain with a binding domain from a second restriction endonuclease or methyltransferase; (c) mutating the N-terminal domain, the C-terminal domain or both domains to alter the binding specificity ; or (d) changing the length of the spacer amino acid sequence between the N-terminal and C-terminal domains of the specificity module. The second restriction endonuclease or methyltransferase is chosen from Type I restriction endonuclease, Type IIG restriction endonuclease and gamma-type m6A methyltransferase. The specificity subunit and the catalytic subunit are encoded by different genes. (I) Comprises sequences such as nnnnnnnnnncaannnnngtggnnnnnnnnnnnnn (SEQ ID No: 32), nnnnnnnnnnncaannnnngtggnnnnnnnnnnnn (SEQ ID No: 33), caannnnngtgg (SEQ ID No: 34), caannngtgg (SEQ ID No: 35), where n=a, c, t or g.

USE - (I) Is useful for generating endonucleases with new specificity, for innovative genetic engineering.

EXAMPLE - CspCI was obtained by culturing either Citrobacter sp. 2144 (NEB#1398) or the transformed host Escherichia coli NEB#1554, and recovering the endonuclease from the cells. Citrobacter sp. 2144 (NEB#1398) or E.coli NEB#1554 were incubated aerobically at 37degreesC. Cells in the late logarithmic stage of growth were collected by centrifugation and either disrupted immediately or stored frozen at -70degreesC. The cell paste was suspended in a buffer solution and ruptured by sonication, high pressure dispersion or enzymatic digestion to allow extraction of the endonuclease by the buffer solution. Intact cells and cellular debris were then removed by centrifugation to produce a cell-free extract containing CspCI. The CspCI endonuclease was then purified from the cell-free extract by ion exchange chromatography, affinity chromatography, molecular sieve chromatography, or their combinations. 277 grams of E.coli NEB#1554 CspCI cell pellet or Citrobacter sp. 2144 were suspended in 1 liter of buffer A containing 300mM sodium chloride, and passed through a Gaulin homogenizer at 12000

psig. The lysate was centrifuged at 13000xG for 40 minutes and the supernatant collected. The supernatant solution was applied to a 400 ml diethylaminoethyl (DEAE) fast flow column. The diluted enzyme was applied to a 375 ml heparin hyper D column. A 2.5 L wash of buffer B was applied, then a 2 L gradient of sodium chloride from 0.15-1M in buffer B was applied and fractions were collected. Fractions were assayed for CspCI endonuclease activity by incubating with 1 microgram of phase lambda DNA (NEB) in 50 mulNEB buffer 2, supplemented with 20 micromolar for 15 minutes at 37degreesC. CspCI activity eluted at 0.3-0.35 M sodium chloride. CspCI activity eluted at 0.4-0.5 M potassium hydrogen phosphate.(87 pages)

L12 ANSWER 115 OF 314 USPATFULL on STN
ACCESSION NUMBER: 2004:280826 USPATFULL
TITLE: Methods and compositions relating to 5'-chimeric ribonucleic acids
INVENTOR(S): Sternberg, Paul, Pasadena, CA, UNITED STATES
Hwang, Byung Joon, San Marino, CA, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 20040220127	A1	20041104
APPLICATION INFO.:	US 2003-639016	A1	20030811 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2002-423490P	20021104 (60)
	US 2002-402473P	20020809 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: ROPES & GRAY LLP, ONE INTERNATIONAL PLACE, BOSTON, MA, 02110-2624
NUMBER OF CLAIMS: 57
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 20 Drawing Page(s)
LINE COUNT: 3314
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The disclosure provides, among other things, methods for producing and using 5'-chimeric RNAs and cDNAs. 5'-chimeric RNAs and cDNAs may be used, for example, for high-throughput analysis of the 5'-end sequences for RNA transcripts.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L12 ANSWER 132 OF 314 USPATFULL on STN
ACCESSION NUMBER: 2004:2072 USPATFULL
TITLE: Hybrid and single chain meganucleases and use thereof
INVENTOR(S): Arnould, Sylvain, Paris, FRANCE
Chames, Patrick, Paris, FRANCE
Choulika, Andre, Paris, FRANCE
Epinat, Jean-Charles, Paris, FRANCE
Lacroix, Emmanuel, Paris, FRANCE

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 20040002092	A1	20040101
APPLICATION INFO.:	US 2003-388230	A1	20030314 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2002-364113P	20020315 (60)

DOCUMENT TYPE: Utility

FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: NIXON & VANDERHYE, PC, 1100 N GLEBE ROAD, 8TH FLOOR, ARLINGTON, VA, 22201-4714
NUMBER OF CLAIMS: 26
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 12 Drawing Page(s)
LINE COUNT: 3746
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This patent application relates to hybrid and/or single-chain rare-cutting endonucleases, called meganucleases, which recognize and cleave a specific nucleotide sequence, to polynucleotide sequences encoding for said rare-cutting endonucleases, to a vector comprising one of said polynucleotide sequences, to a cell or animal comprising one of said polynucleotide sequences or said rare-cutting endonucleases, to a process for producing one of said rare-cuuting endonucleases and any use of the disclosed products and methods. More particularly, this invention contemplates any use of such rare-cutting endonuclease for genetic engineering and gene therapy.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L12 ANSWER 197 OF 314 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
ACCESSION NUMBER: 2002:585532 BIOSIS
DOCUMENT NUMBER: PREV200200585532
TITLE: Type I restriction-modification systems from Lactobacillus delbrueckii subsp. lactis.
AUTHOR(S): Bourniquel, A. A. [Reprint author]; Mollet, B.; Bickle, T. A. [Reprint author]
CORPORATE SOURCE: Biozentrum, Univ. of Basel, Basel, Switzerland
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 238. print.
Meeting Info.: 102nd General Meeting of the American Society for Microbiology. Salt Lake City, UT, USA. May 19-23, 2002. American Society for Microbiology.
ISSN: 1060-2011.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 13 Nov 2002
Last Updated on STN: 13 Nov 2002
AB Background: Lactobacillus delbrueckii subsp. lactis is a lactic acid bacterium used worldwide for the production of Swiss-type hard cheeses. Whereas other dairy starters, e.g. Lactococcus lactis or Streptococcus thermophilus, are highly susceptible to bacteriophage infections, very few phages are known to target L. delbrueckii ssp. suggesting these bacteria possess a very active and reliable/versatile endogenous defense mechanism. Type I restriction-modification (R-M) systems are acknowledged defense mechanisms that depend on the generation of novel specificities for adaptability. Methods: Type I R-M hsd (host specificity for DNA) gene clusters were isolated from two strains of L. delbrueckii subsp. lactis, sequenced and characterized. In vivo transcription of the identified genes was verified by Northern blotting. The hsdR (restriction), hsdM (modification) and hsdS (specificity of DNA binding)
genes were cloned into expression vectors for overexpression in Escherichia coli. The expressed proteins were purified, tested for activity and their recognition sites determined. Results: Both L. delbrueckii subsp. lactis strains examined possess type I R-M systems. The two hsd clusters (apprx8 kb) share a similar genetic organization consisting of: (i) the hsdR, hsdM and hsdS genes coding for a type I restriction enzyme, (ii) a second hsdS
gene with a truncated 5'-end, and (iii) a gene similar to phage

integrases. The HsdR and HsdM snbunits on both strains are highly conserved (98% identity), whereas the hsds genes code for subunits with different specificities i.e. the two type I restriction enzymes have different recognition sites. Conclusion: Until recently, research on type I R-M systems focused on the enterobacteriaceae group in which hsd genes are but slightly conserved in-between strains. In the gram-positive bacterium L. delbrueckii subsp. lactis type I R-M genes are well-conserved, genetic variability being limited to the DNA binding domains of hsdS determining enzyme specificity. The presence of truncated hsdS and integrases genes in the hsd clusters suggests that novel specificities might be generated by domain shuffling.

L12 ANSWER 208 OF 314 BIOTECHNO COPYRIGHT 2009 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2001:33116733 BIOTECHNO
TITLE: DNA cleavage by type III restriction-modification enzyme EcoP15I is independent of spacer distance between two head to head oriented recognition sites
AUTHOR: Mucke M.; Reich S.; Moncke-Buchner E.; Reuter M.; Kruger D.H.
CORPORATE SOURCE: D.H. Kruger, Institut fur Virologie, Medizinische Fakultat (Charite), Humboldt-Universitat zu Berlin, D-10098, Berlin, Germany.
E-mail: detlev.kruger@charite.de
SOURCE: Journal of Molecular Biology, (28 SEP 2001), 312/4 (687-698), 42 reference(s)
CODEN: JMOBAK ISSN: 0022-2836
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2001:33116733 BIOTECHNO
AB The type III restriction-modification enzyme EcoP15I requires the interaction of two unmethylated, inversely oriented recognition sites 5'-CAG-CAG in head to head configuration to allow an efficient DNA cleavage. It has been hypothesized that two convergent DNA-translocating enzyme-substrate complexes interact to form the active cleavage complex and that translocation is driven by ATP hydrolysis. Using a half-automated, fluorescence-based detection method, we investigated how the distance between two inversely oriented recognition sites affects DNA cleavage efficiency. We determined that EcoP15I cleaves DNA efficiently even for two adjacent head to head or tail to tail oriented target sites. Hence, DNA translocation appears not to be required for initiating DNA cleavage in these cases. Furthermore, we report here that EcoP15I is able to cleave single-site substrates. When we analyzed the interaction of EcoP15I with DNA substrates containing adjacent target sites in the presence of non-hydrolyzable ATP analogues, we found that cleavage depended on the hydrolysis of ATP. Moreover, we show that cleavage occurs at only one of the two possible cleavage positions of an interacting pair of target sequences. When EcoP15I bound to a DNA substrate containing one recognition site in the absence of ATP, we observed a 36 nucleotide DNaseI-footprint that is asymmetric on both strands. All of our footprinting experiments showed that the enzyme did not cover the region around the cleavage site. Analyzing a DNA fragment with two head to head oriented recognition sites, EcoP15I protected 27-33 nucleotides around the recognition sequence, including an additional region of 26 bp between both cleavage sites. For all DNA substrates examined, the presence of ATP caused altered foot-printing patterns. We assume that the altered patterns are most likely due to a conformational change of the enzyme. Overall, our data further refine the tracking-collision model for type III restriction enzymes. .COPYRGT. 2001 Academic Press.

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L12 ANSWER 106 OF 314 BIOTECHDS COPYRIGHT 2009 THOMSON REUTERS on STN
ACCESSION NUMBER: 2005-29788 BIOTECHDS
TITLE: New pure Type IIG restriction endonuclease obtainable from Citrobacter species or from Escherichia coli, useful for generating restriction endonucleases with new specificities; for use in genetic engineering
AUTHOR: MORGAN R; WILSON G; LUNNEN K; HEITER D; BENNER J; NKENFOU C N; PICONE S
PATENT ASSIGNEE: NEW ENGLAND BIOLABS INC
PATENT INFO: WO 2005094516 13 Oct 2005
APPLICATION INFO: WO 2005-US9824 23 Mar 2005
PRIORITY INFO: US 2004-555796 24 Mar 2004; US 2004-555796 24 Mar 2004
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2005-714328 [73]
AN 2005-29788 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - A substantially pure Type IIG restriction endonuclease (I) obtainable from Citrobacter sp. 2144 (NEB#1398) (American Type Culture Collection (ATCC) Patent Accession Number PTA-5846) or from Escherichia coli NEB#1554 (ATCC Patent Accession Number PTA-5887), is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) an isolated DNA obtainable from Citrobacter sp. 2144 (NEB (2) 1398) (ATCC Patent Accession Number PTA-5846) or from E.coli NEB (3) 1554 (ATCC Patent Accession Number PTA-5887) and encoding (I), where the DNA comprises a first DNA segment expressing an endonuclease and methyl transferase catalytic function and a second DNA segment encoding a sequence specificity function of the restriction endonuclease, where the first and second DNA segments comprise one or more DNA molecules; (4) a recombinant DNA vector comprising at least one of first DNA segment coding for the restriction and modification domains of CspCI restriction endonuclease and a second segment coding for the specificity domain of the restriction endonuclease; (5) a host cell (II) transformed with a first DNA segment coding for the restriction and modification domains of CspCI restriction endonuclease and a second segment coding for the specificity domain of the restriction endonuclease, where the first DNA segment and the second DNA segment are contained with one or more DNA vectors; (6) preparing (I); and (7) making (M1) Type II restriction endonuclease having an altered specificity comprising: (a) selecting a restriction endonuclease from a set of enzymes, where each enzyme in the set is characterized by a modular structure having a specificity subunit and a catalytic subunit, the specificity subunit further comprising N-terminal domain for binding one half site of a bipartite recognition sequence and a C-terminal domain for binding a second half site of the bipartite recognition sequence; (b) modifying the specificity subunit; and (c) obtaining the Type II restriction endonuclease with altered specificity.

BIOTECHNOLOGY - Preparation: Preparing (I), involves cultivating a

sample of Citrobacter sp. 2144 (NEB#1398) or (II) under conditions favoring the production of the endonuclease, and purifying the endonuclease (claimed). Preferred Endonuclease: (I) Is capable of recognizing at least one sequence chosen (SEQ ID No: 32-35), and cleaving the DNA on both sides of the recognition sequence. Preferred Method: In (M1), modifying the specificity subunit further comprises: (a) substituting the N-terminal domain with a second C-terminal domain or substituting the C-terminal domain with a second N-terminal domain; (b) substituting the N-terminal domain or the C-terminal domain or both N-terminal and C-terminal domain with a binding domain from a second restriction endonuclease or methyltransferase; (c) mutating the N-terminal domain, the C-terminal domain or both domains to alter the binding specificity ; or (d) changing the length of the spacer amino acid sequence between the N-terminal and C-terminal domains of the specificity module. The second restriction endonuclease or methyltransferase is chosen from Type I restriction endonuclease, Type IIG restriction endonuclease and gamma-type m6A methyltransferase. The specificity subunit and the catalytic subunit are encoded by different genes. (I) Comprises sequences such as nnnnnnnnnncaannnnngtggnnnnnnnnnnnnnn (SEQ ID No: 32), nnnnnnnnnnncaannnnngtggnnnnnnnnnnnn (SEQ ID No: 33), caannnnngtgg (SEQ ID No: 34), caannnngtgg (SEQ ID No: 35), where n=a, c, t or g.

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EXAMPLE - CspCI was obtained by culturing either Citrobacter sp. 2144 (NEB#1398) or the transformed host Escherichia coli NEB#1554, and recovering the endonuclease from the cells. Citrobacter sp. 2144 (NEB#1398) or E.coli NEB#1554 were incubated aerobically at 37degreesC. Cells in the late logarithmic stage of growth were collected by centrifugation and either disrupted immediately or stored frozen at -70degreesC. The cell paste was suspended in a buffer solution and ruptured by sonication, high pressure dispersion or enzymatic digestion to allow extraction of the endonuclease by the buffer solution. Intact cells and cellular debris were then removed by centrifugation to produce a cell-free extract containing CspCI. The CspCI endonuclease was then purified from the cell-free extract by ion exchange chromatography, affinity chromatography, molecular sieve chromatography, or their combinations. 277 grams of E.coli NEB#1554 CspCI cell pellet or Citrobacter sp. 2144 were suspended in 1 liter of buffer A containing 300mM sodium chloride, and passed through a Gaulin homogenizer at 12000 psig. The lysate was centrifuged at 13000xG for 40 minutes and the supernatant collected. The supernatant solution was applied to a 400 ml diethylaminoethyl (DEAE) fast flow column. The diluted enzyme was applied to a 375 ml heparin hyper D column. A 2.5 L wash of buffer B was applied, then a 2 L gradient of sodium chloride from 0.15-1M in buffer B was applied and fractions were collected. Fractions were assayed for CspCI endonuclease activity by incubating with 1 microgram of phase lambda DNA (NEB) in 50 mulNEB buffer 2, supplemented with 20 micromolar for 15 minutes at 37degreesC. CspCI activity eluted at 0.3-0.35 M sodium chloride. CspCI activity eluted at 0.4-0.5 M potassium hydrogen phosphate.(87 pages)

L12 ANSWER 115 OF 314 USPATFULL on STN
ACCESSION NUMBER: 2004:280826 USPATFULL
TITLE: Methods and compositions relating to 5'-chimeric ribonucleic acids
INVENTOR(S): Sternberg, Paul, Pasadena, CA, UNITED STATES
Hwang, Byung Joon, San Marino, CA, UNITED STATES

NUMBER	KIND	DATE

PATENT INFORMATION: US 20040220127 A1 20041104
APPLICATION INFO.: US 2003-639016 A1 20030811 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2002-423490P	20021104 (60)
	US 2002-402473P	20020809 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: ROPES & GRAY LLP, ONE INTERNATIONAL PLACE, BOSTON, MA, 02110-2624
NUMBER OF CLAIMS: 57
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 20 Drawing Page(s)
LINE COUNT: 3314
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The disclosure provides, among other things, methods for producing and using 5'-chimeric RNAs and cDNAs. 5'-chimeric RNAs and cDNAs may be used, for example, for high-throughput analysis of the 5'-end sequences for RNA transcripts.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L12 ANSWER 132 OF 314 USPATFULL on STN
ACCESSION NUMBER: 2004:2072 USPATFULL
TITLE: Hybrid and single chain meganucleases and use thereof
INVENTOR(S): Arnould, Sylvain, Paris, FRANCE
Chames, Patrick, Paris, FRANCE
Choulika, Andre, Paris, FRANCE
Epinat, Jean-Charles, Paris, FRANCE
Lacroix, Emmanuel, Paris, FRANCE

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 20040002092	A1	20040101
APPLICATION INFO.:	US 2003-388230	A1	20030314 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2002-364113P	20020315 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: NIXON & VANDERHYE, PC, 1100 N GLEBE ROAD, 8TH FLOOR, ARLINGTON, VA, 22201-4714
NUMBER OF CLAIMS: 26
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 12 Drawing Page(s)
LINE COUNT: 3746
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This patent application relates to hybrid and/or single-chain rare-cutting endonucleases, called meganucleases, which recognize and cleave a specific nucleotide sequence, to polynucleotide sequences encoding for said rare-cutting endonucleases, to a vector comprising one of said polynucleotide sequences, to a cell or animal comprising one of said polynucleotide sequences or said rare-cutting endonucleases, to a process for producing one of said rare-cuuting endonucleases and any use of the disclosed products and methods. More particularly, this invention contemplates any use of such rare-cutting endonuclease for genetic engineering and gene therapy.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L12 ANSWER 197 OF 314 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

ACCESSION NUMBER: 2002:585532 BIOSIS
DOCUMENT NUMBER: PREV200200585532
TITLE: Type I restriction-modification systems from Lactobacillus delbrueckii subsp. lactis.
AUTHOR(S): Bourniquel, A. A. [Reprint author]; Mollet, B.; Bickle, T. A. [Reprint author]
CORPORATE SOURCE: Biozentrum, Univ. of Basel, Basel, Switzerland
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 238. print.
Meeting Info.: 102nd General Meeting of the American Society for Microbiology. Salt Lake City, UT, USA. May 19-23, 2002. American Society for Microbiology.
ISSN: 1060-2011.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 13 Nov 2002
Last Updated on STN: 13 Nov 2002

AB Background: Lactobacillus delbrueckii subsp. lactis is a lactic acid bacterium used worldwide for the production of Swiss-type hard cheeses. Whereas other dairy starters, e.g. Lactococcus lactis or Streptococcus thermophilus, are highly susceptible to bacteriophage infections, very few phages are known to target L. delbrueckii ssp. suggesting these bacteria possess a very active and reliable/versatile endogenous defense mechanism. Type I restriction-modification (R-M) systems are acknowledged defense mechanisms that depend on the generation of novel specificities for adaptability. Methods: Type I R-M hsd (host specificity for DNA) gene clusters were isolated from two strains of L. delbrueckii subsp. lactis, sequenced and characterized. In vivo transcription of the identified genes was verified by Northern blotting. The hsdR (restriction), hsdM (modification) and hsdS (specificity of DNA binding)
genes were cloned into expression vectors for overexpression in Escherichia coli. The expressed proteins were purified, tested for activity and their recognition sites determined. Results: Both L. delbrueckii subsp. lactis strains examined possess type I R-M systems. The two hsd clusters (apprx8 kb) share a similar genetic organization consisting of: (i) the hsdR, hsdM and hsdS genes coding for a type I restriction enzyme, (ii) a second hsdS
gene with a truncated 5'-end, and (iii) a gene similar to phage integrases. The HsdR and HsdM snbunits on both strains are highly conserved (98% identity), whereas the hsds genes code for subunits with different specificities i.e. the two type I restriction enzymes have different recognition sites. Conclusion: Until recently, research on type I R-M systems focused on the enterobacteriaceae group in which hsd genes are but slightly conserved in-between strains. In the gram-positive bacterium L. delbrueckii subsp. lactis type I R-M genes are well-conserved, genetic variability being limited to the DNA binding domains of hsdS determining enzyme specificity. The presence of truncated hsdS and integrases genes in the hsd clusters suggests that novel specificities might be generated by domain shuffling.

L12 ANSWER 208 OF 314 BIOTECHNO COPYRIGHT 2009 Elsevier Science B.V. on STN

ACCESSION NUMBER: 2001:33116733 BIOTECHNO
TITLE: DNA cleavage by type III restriction-modification enzyme EcoP15I is independent of spacer distance between two head to head oriented recognition sites
AUTHOR: Mucke M.; Reich S.; Moncke-Buchner E.; Reuter M.; Kruger D.H.
CORPORATE SOURCE: D.H. Kruger, Institut fur Virologie, Medizinische Fakultat (Charite), Humboldt-Universitat zu Berlin,

D-10098, Berlin, Germany.
E-mail: detlev.kruger@charite.de
SOURCE: Journal of Molecular Biology, (28 SEP 2001), 312/4 (687-698), 42 reference(s)
CODEN: JMOBAK ISSN: 0022-2836
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2001:33116733 BIOTECHNO
AB The type III restriction-modification enzyme EcoP15I requires the interaction of two unmethylated, inversely oriented recognition sites 5'-CAG-CAG in head to head configuration to allow an efficient DNA cleavage. It has been hypothesized that two convergent DNA-translocating enzyme-substrate complexes interact to form the active cleavage complex and that translocation is driven by ATP hydrolysis. Using a half-automated, fluorescence-based detection method, we investigated how the distance between two inversely oriented recognition sites affects DNA cleavage efficiency. We determined that EcoP15I cleaves DNA efficiently even for two adjacent head to head or tail to tail oriented target sites. Hence, DNA translocation appears not to be required for initiating DNA cleavage in these cases. Furthermore, we report here that EcoP15I is able to cleave single-site substrates. When we analyzed the interaction of EcoP15I with DNA substrates containing adjacent target sites in the presence of non-hydrolyzable ATP analogues, we found that cleavage depended on the hydrolysis of ATP. Moreover, we show that cleavage occurs at only one of the two possible cleavage positions of an interacting pair of target sequences. When EcoP15I bound to a DNA substrate containing one recognition site in the absence of ATP, we observed a 36 nucleotide DNaseI-footprint that is asymmetric on both strands. All of our footprinting experiments showed that the enzyme did not cover the region around the cleavage site. Analyzing a DNA fragment with two head to head oriented recognition sites, EcoP15I protected 27-33 nucleotides around the recognition sequence, including an additional region of 26 bp between both cleavage sites. For all DNA substrates examined, the presence of ATP caused altered foot-printing patterns. We assume that the altered patterns are most likely due to a conformational change of the enzyme. Overall, our data further refine the tracking-collision model for type III restriction enzymes. .COPYRGT. 2001 Academic Press.
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L12 ANSWER 208 OF 314 BIOTECHNO COPYRIGHT 2009 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2001:33116733 BIOTECHNO
TITLE: DNA cleavage by type III restriction-modification enzyme EcoP15I is independent of spacer distance between two head to head oriented recognition sites
AUTHOR: Mucke M.; Reich S.; Moncke-Buchner E.; Reuter M.; Kruger D.H.
CORPORATE SOURCE: D.H. Kruger, Institut fur Virologie, Medizinische Fakultat (Charite), Humboldt-Universitat zu Berlin, D-10098, Berlin, Germany.
E-mail: detlev.kruger@charite.de
SOURCE: Journal of Molecular Biology, (28 SEP 2001), 312/4 (687-698), 42 reference(s)

CODEN: JMOBAK ISSN: 0022-2836
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2001:33116733 BIOTECHNO
AB The type III restriction-modification enzyme EcoP15I requires the interaction of two unmethylated, inversely oriented recognition sites 5'-CAG-CAG in head to head configuration to allow an efficient DNA cleavage. It has been hypothesized that two convergent DNA-translocating enzyme-substrate complexes interact to form the active cleavage complex and that translocation is driven by ATP hydrolysis. Using a half-automated, fluorescence-based detection method, we investigated how the distance between two inversely oriented recognition sites affects DNA cleavage efficiency. We determined that EcoP15I cleaves DNA efficiently even for two adjacent head to head or tail to tail oriented target sites. Hence, DNA translocation appears not to be required for initiating DNA cleavage in these cases. Furthermore, we report here that EcoP15I is able to cleave single-site substrates. When we analyzed the interaction of EcoP15I with DNA substrates containing adjacent target sites in the presence of non-hydrolyzable ATP analogues, we found that cleavage depended on the hydrolysis of ATP. Moreover, we show that cleavage occurs at only one of the two possible cleavage positions of an interacting pair of target sequences. When EcoP15I bound to a DNA substrate containing one recognition site in the absence of ATP, we observed a 36 nucleotide DNaseI-footprint that is asymmetric on both strands. All of our footprinting experiments showed that the enzyme did not cover the region around the cleavage site. Analyzing a DNA fragment with two head to head oriented recognition sites, EcoP15I protected 27-33 nucleotides around the recognition sequence, including an additional region of 26 bp between both cleavage sites. For all DNA substrates examined, the presence of ATP caused altered foot-printing patterns. We assume that the altered patterns are most likely due to a conformational change of the enzyme. Overall, our data further refine the tracking-collision model for type III restriction enzymes. .COPYRGT. 2001 Academic Press.
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AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 00:50:04 ON 01 FEB 2009
SEA (RESTRIC?(3A)ENDONUCLEAS?) OR (RESTRIC?(3A)ENZYM?) OR (REST

21	FILE ADISCTI
3	FILE ADISINSIGHT
7	FILE ADISNEWS
3845	FILE AGRICOLA
104	FILE ANABSTR
42	FILE ANTE
40	FILE AQUALINE
1189	FILE AQUASCI
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31117	FILE BIOSIS
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10212	FILE BIOTECHDS
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338	FILE CONFSCI
3	FILE CROPB
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43989	FILE DGENE
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425	FILE DRUGU
88	FILE EMBAL
21832	FILE EMBASE
9157	FILE ESBIOBASE
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66	FILE PHIN
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3	FILE RDISCLOSURE
20911	FILE SCISEARCH
10529	FILE TOXCENTER
14486	FILE USGENE
72194	FILE USPATFULL
29	FILE USPATOLD
11872	FILE USPAT2
1	FILE VETB
144	FILE VETU

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              62   FILE WATER
            9109   FILE WPIDS
              62   FILE WPIFV
            9109   FILE WPINDEX
              37   FILE IPA
               4   FILE NAPRALERT
             488   FILE NLDB
L1              QUE (RESTRIC?(3A) ENDONUCLEAS?) OR (RESTRIC?(3A) ENZYM?) OR
                (RESTRIC?(3A) MODIF?(5A)(ENZYM? OR ENDONUCLEAS? OR SYSTEM?))
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                D RANK

     FILE 'USPATFULL, CAPLUS, MEDLINE, BIOSIS, EMBASE, SCISEARCH, LIFESCI,
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     01:00:54 ON 01 FEB 2009
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L3           79162 SEA L2(S)(SPECIFI? OR RECOG?)(S)(SEQUENC? OR DNA?)
L4           49041 SEA L3 AND (HYBRID? OR RECOMBINAT? OR TRUNCAT? OR TRANSPOS?)
L5             990 SEA L3(S)((TWO(3A) RECOGNIT?(3A) SITE?) OR HSDS?)
L6             344 SEA L5 (S)(HYBRID? OR RECOMBIN? OR TRUNCA? OR EXCHANG? OR
                   TRANSPOS? OR ALTER?)
L7             280 DUP REM L6 (64 DUPLICATES REMOVED)
L8              14 SEA L7(S) HALF?
                   D TI L8 1-14
                   D L8 IBIB ABS 8 12 13
L9            1657 SEA L2(S)((TWO(3A) RECOG?(3A) SITE?) OR HSDS? OR (HALF?(3A)
                   SITE?))
L10            500 SEA L9(S)(HYBRID? OR RECOMB? OR TRUNC? OR EXCH? OR TRANSPO? OR
                   ALTER?)
L11            359 SEA L10 AND ((MODIF? OR ALTER? OR HYBRID?)(3A)(DNA? OR SEQUEN?
                   OR SPECIFIC? OR (RECOGN?(3A) SITE?)))
L12            314 DUP REM L11 (45 DUPLICATES REMOVED)
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                   D IBIB ABS L12 106 115 132 197 208 221 267 269 278 282 283 314
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     FILE STNINDEX

     FILE USPATFULL
     FILE COVERS 1971 TO PATENT PUBLICATION DATE: 29 Jan 2009 (20090129/PD)
     FILE LAST UPDATED: 29 Jan 2009 (20090129/ED)
     HIGHEST GRANTED PATENT NUMBER: US7484247
     HIGHEST APPLICATION PUBLICATION NUMBER: US20090031463
     CA INDEXING IS CURRENT THROUGH 29 Jan 2009 (20090129/UPCA)
     ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 29 Jan 2009 (20090129/PD)
     REVISED CLASS FIELDS (/NCL) LAST RELOADED: Dec 2008
     USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Dec 2008

     USPATFULL now includes complete International Patent Classification (IPC)
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FILE COVERS 1907 - 1 Feb 2009 VOL 150 ISS 6
FILE LAST UPDATED: 29 Jan 2009 (20090129/ED)

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FILE MEDLINE
FILE LAST UPDATED: 31 Jan 2009 (20090131/UP). FILE COVERS 1949 TO DATE.

MEDLINE and LMEDLINE have been updated with the 2009 Medical Subject Headings (MeSH) vocabulary and tree numbers from the U.S. National Libra of Medicine (NLM). Additional information is available at

http://www.nlm.nih.gov/pubs/techbull/nd08/nd08_medline_data_changes_2009.

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See HELP RANGE before carrying out any RANGE search.

MEDLINE Accession Numbers (ANs) for records from 1950-1977 have been converted from 8 to 10 digits. Searches using an 8 or 10 digit AN will retrieve the same record. The 10-digit ANs can be expanded, searched, and displayed in all records from 1949 to the present.

FILE BIOSIS
FILE COVERS 1926 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT FROM JANUARY 1926 TO DATE.

RECORDS LAST ADDED: 28 January 2009 (20090128/ED)

BIOSIS has been augmented with 1.8 million archival records from 1926 through 1968. These records have been re-indexed to match current BIOSIS indexing.

FILE EMBASE
FILE COVERS 1974 TO 30 Jan 2009 (20090130/ED)

EMBASE was reloaded on March 30, 2008.

EMBASE is now updated daily. SDI frequency remains weekly (default) and biweekly.

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FILE SCISEARCH

FILE COVERS 1974 TO 29 Jan 2009 (20090129/ED)

SCISEARCH has been reloaded, see HELP RLOAD for details.

FILE LIFESCI
FILE COVERS 1978 TO 20 Jan 2009 (20090120/ED)

FILE BIOTECHNO
FILE LAST UPDATED: 7 JAN 2004 <20040107/UP>
FILE COVERS 1980 TO 2003.
THIS FILE IS A STATIC FILE WITH NO UPDATES

>>> SIMULTANEOUS LEFT AND RIGHT TRUNCATION AVAILABLE IN /CT AND BASIC INDEX <<<

FILE USGENE
FILE LAST UPDATED: 30 JAN 2009 <20090130/UP>
MOST RECENT PUBLICATION DATE: 15 JAN 2009 <20090115/PD>
FILE COVERS 1982 TO DATE

>>> SIMULTANEOUS LEFT AND RIGHT TRUNCATION (SLART) IS AVAILABLE IN THE BASIC INDEX (/BI) AND FEATURE TABLE (/FEAT) FIELDS <<<

>>> DOWNLOAD THE USGENE WORKSHOP MANUAL:
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http://www.stn-international.com/New_sequence_search.html <<<

FILE PASCAL
FILE LAST UPDATED: 26 JAN 2009 <20090126/UP>
FILE COVERS 1977 TO DATE.

>>> SIMULTANEOUS LEFT AND RIGHT TRUNCATION IS AVAILABLE IN THE BASIC INDEX (/BI) FIELD <<<

FILE USPAT2

FILE COVERS 2001 TO PUBLICATION DATE: 29 Jan 2009 (20090129/PD)
FILE LAST UPDATED: 29 Jan 2009 (20090129/ED)

HIGHEST GRANTED PATENT NUMBER: US20080088069
HIGHEST APPLICATION PUBLICATION NUMBER: US20090030948
CA INDEXING IS CURRENT THROUGH 29 Jan 2009 (20090129/UPCA)
ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 29 Jan 2009 (20090129/PD)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Dec 2008
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Dec 2008

USPAT2 now includes complete International Patent Classification (IPC) reclassification data for the third quarter of 2008.

FILE TOXCENTER

FILE COVERS 1907 TO 27 Jan 2009 (20090127/ED)

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FILE CABA
FILE COVERS 1973 TO 8 Jan 2009 (20090108/ED)

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FILE BIOTECHDS
FILE LAST UPDATED: 12 JAN 2009 <20090112/UP>
FILE COVERS 1982 TO DATE

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=> d ibib abs l12 283

L12 ANSWER 283 OF 314 LIFESCI COPYRIGHT 2009 CSA on STN DUPLICATE 31
ACCESSION NUMBER: 84:97138 LIFESCI
TITLE: Genetic recombination can generate altered restriction specificity.
AUTHOR: Fuller-Pace, F.V.; Bullas, L.R.; Delius, H.; Murray, N.E.
CORPORATE SOURCE: Dep. Mol. Biol., Univ. Edinburgh, King's Build., Mayfield Rd., Edinburgh EH9 3JR, UK
SOURCE: PROC. NATL. ACAD. SCI. USA., (1984) vol. 81, no. 19, pp. 6095-6099.
DOCUMENT TYPE: Journal
FILE SEGMENT: N; G
LANGUAGE: English
SUMMARY LANGUAGE: English
AB A recombinant strain, isolated following the transduction of an Escherichia coli recipient carrying the Salmonella typhimurium (SB) specificity genes with DNA from a donor having the Salmonella potsdam (SP) specificity, was shown to have neither SB nor SP specificity but to encode a novel restriction specificity, SQ. The heteroduplex analysis of the hsdS (specificity) genes of the SB and SP restriction and modification systems described here identifies a conserved sequence of around 100 base pairs flanked by two nonhomologous regions each of approximately 500 base pairs. The